

SEQUENCE LISTING

<110> NIIGATA TLO CORPORATION

<120> Vector for gene therapy and method for quantifying target protein in mammal or cultured cell to which the vector for gene therapy was administered

<130> 03PF275-PCT

<150> JP 2003-3967

<151> 2003-01-10

<160> 24

<210> 1

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> oligopeptide encoding C19-29 region of glucagon of human, mouse or rat

<400> 1

Ala Gln Asp Phe Val Gln Trp Leu Met Asn Thr

1 5 10

<210> 2

<211> 1471

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (13)..(1461)

<223> DNA insert encoding rat IFN- γ receptor, rat IgG Fc region and glucagon C19-29 region

<400> 2

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 Met Ile Leu Leu Val Val Leu Met Leu Ser Ala Glu Ile

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ggg agt gga gct ttg atg agc acc gag gat cct aag ccg ccc tcg gtg 99
 Gly Ser Gly Ala Leu Met Ser Thr Glu Asp Pro Lys Pro Pro Ser Val
 15 20 25

cct gcg cca aca aat gtt cta att acg tcc tat gac ttg aac cct gtc 147
 Pro Ala Pro Thr Asn Val Leu Ile Thr Ser Tyr Asp Leu Asn Pro Val
 30 35 40 45

gta cat tgg aag cac cag aac gtg tcg cag gct gcc gtc ttc act gta 195
 Val His Trp Lys His Gln Asn Val Ser Gln Ala Ala Val Phe Thr Val
 50 55 60

cag gta aag atg tat cca gaa tac tgg act gat gcc tgc acc aac att 243
 Gln Val Lys Met Tyr Pro Glu Tyr Trp Thr Asp Ala Cys Thr Asn Ile
 65 70 75

gcc cat cat tat tgt aat atc tac aaa cac att tcc tat cct gac tca 291
 Ala His His Tyr Cys Asn Ile Tyr Lys His Ile Ser Tyr Pro Asp Ser
 80 85 90

tct gcc tgg gcc aga gtt aag gcc aag gtt gga caa aga gaa tct gcc 339
 Ser Ala Trp Ala Arg Val Lys Ala Lys Val Gly Gln Arg Glu Ser Ala
 95 100 105

tat gcg cag tca gaa gag ttt att atg tgc cga aag ggg aag gtt gga 387
 Tyr Ala Gln Ser Glu Glu Phe Ile Met Cys Arg Lys Gly Lys Val Gly
 110 115 120 125

ccg cct ggc ctg gac atc gga agg aag gaa gat cag ctg att gtc cac 435
 Pro Pro Gly Leu Asp Ile Gly Arg Lys Glu Asp Gln Leu Ile Val His

| 130 | 135 | 140 | |
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| ata ttt cac cct aag gtc aat gtg agt cag gaa acc atg ttt ggt gac Ile Phe His Pro Lys Val Asn Val Ser Gln Glu Thr Met Phe Gly Asp | | | 483 |
| 145 | 150 | 155 | |
| gga aat acc tgt tac aca ttc gac tac act gtg ttt gtg aaa cat tac Gly Asn Thr Cys Tyr Thr Phe Asp Tyr Thr Val Phe Val Lys His Tyr | | | 531 |
| 160 | 165 | 170 | |
| agg agt ggg gag atc cta cat aca gaa cat agc gtc cta aaa gaa gat Arg Ser Gly Glu Ile Leu His Thr Glu His Ser Val Leu Lys Glu Asp | | | 579 |
| 175 | 180 | 185 | |
| tgt agc gaa act ctg tgt gag tta aac atc tca gtg tcc acg ctg aat Cys Ser Glu Thr Leu Cys Glu Leu Asn Ile Ser Val Ser Thr Leu Asn | | | 627 |
| 190 | 195 | 200 | 205 |
| tcc aat tac tgt gtt tca gta gtt gga aag tcg tct ttc tgg caa gtt Ser Asn Tyr Cys Val Ser Val Val Gly Lys Ser Ser Phe Trp Gln Val | | | 675 |
| 210 | 215 | 220 | |
| aat aca gaa aca tca aaa gac gcc tgt atc ccc ttt ctc cat gat gac Asn Thr Glu Thr Ser Lys Asp Ala Cys Ile Pro Phe Leu His Asp Asp | | | 723 |
| 225 | 230 | 235 | |
| aga gaa gaa gcg gcc gcc gtg ccc aga aac tgt gga ggt gat tgc aag Arg Glu Glu Ala Ala Ala Val Pro Arg Asn Cys Gly Gly Asp Cys Lys | | | 771 |
| 240 | 245 | 250 | |
| cct tgt ata tgt aca ggc tca gaa gta tca tct gtc ttc atc ttc ccc Pro Cys Ile Cys Thr Gly Ser Glu Val Ser Ser Val Phe Ile Phe Pro | | | 819 |
| 255 | 260 | 265 | |
| cca aag ccc aaa gat gtg ctc acc atc act ctg act cct aag gtc acg Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr Pro Lys Val Thr | | | 867 |

| | | | | |
|--|-----|-----|-----|------|
| 270 | 275 | 280 | 285 | |
| | | | | 915 |
| tgt gtt gtg gta gac att agc cag gag gat ccc gag gtc cat ttc agc Cys Val Val Val Asp Ile Ser Gln Asp Asp Pro Glu Val His Phe Ser | | | | |
| 290 | 295 | 300 | | |
| | | | | 963 |
| tgg ttt gta gat gac gtg gaa gtc cac aca gct cag act cga cca cca Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln Thr Arg Pro Pro | | | | |
| 305 | 310 | 315 | | |
| | | | | 1011 |
| gag gag cag ttc aac agc act ttc cgc tca gtc agt gaa ctc ccc atc Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser Glu Leu Pro Ile | | | | |
| 320 | 325 | 330 | | |
| | | | | 1059 |
| ctg cac cag gac tgg ctc aat ggc agg acg ttc aga tgc aag gtc acc Leu His Gln Asp Trp Leu Asn Gly Arg Thr Phe Arg Cys Lys Val Thr | | | | |
| 335 | 340 | 345 | | |
| | | | | 1107 |
| agt gca gct ttc cca tcc ccc atc gag aaa acc atc tcc aaa ccc gaa Ser Ala Ala Phe Pro Ser Pro Ile Glu Lys Thr Ile Ser Lys Pro Glu | | | | |
| 350 | 355 | 360 | 365 | |
| | | | | 1155 |
| ggc aga aca caa gtt ccg cat gta tac acc atg tca cct acc aag gaa Gly Arg Thr Gln Val Pro His Val Tyr Thr Met Ser Pro Thr Lys Glu | | | | |
| 370 | 375 | 380 | | |
| | | | | 1203 |
| gag atg acc cag aat gaa gtc agt atc acc tgc atg gta aaa ggc ttc Glu Met Thr Gln Asn Glu Val Ser Ile Thr Cys Met Val Lys Gly Phe | | | | |
| 385 | 390 | 395 | | |
| | | | | 1251 |
| tat ccc cca gac att tat gtg gag tgg cag atg aac ggg cag cca cag Tyr Pro Pro Asp Ile Tyr Val Glu Trp Gln Met Asn Gly Gln Pro Gln | | | | |
| 400 | 405 | 410 | | |
| | | | | 1299 |
| gaa aac tac aag aac act cca cct acg atg gac aca gat ggg agt tac Glu Asn Tyr Lys Asn Thr Pro Pro Thr Met Asp Thr Asp Gly Ser Tyr | | | | |

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|--|-----|-----|------|
| 415 | 420 | 425 | |
| | | | |
| ttc ctc tac agc aag ctc aat gtg aag aag gaa aaa tgg cag cag gga Phe Leu Tyr Ser Lys Leu Asn Val Lys Lys Glu Lys Trp Gln Gln Gly | | | 1347 |
| 430 | 435 | 440 | 445 |
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| aac acg ttc acg tgt tct gtg ctg cat gaa ggc ctg cac aac cac cat Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu His Asn His His | | | 1395 |
| 450 | 455 | 460 | |
| | | | |
| act gag aag agt ctc tcc cac tct ccg ggt aaa gcc caa gat ttt gtg Thr Glu Lys Ser Leu Ser His Ser Pro Gly Lys Ala Gln Asp Phe Val | | | 1443 |
| 465 | 470 | 475 | |
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| cag tgg ttg atg aat acc tgagaattct Gln Trp Leu Met Asn Thr | | | 1471 |
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| <212> DNA | | | |
| <213> Artificial Sequence | | | |
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| <223> DNA sequence of artificial expression vector pCAGGS | | | |
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| gcccatatat ggagttccgc gttacataac ttacgtaaa tggccgcct ggctgaccgc | | | 120 |
| ccaacgaccc ccccccattg acgtcaataa tgacgtatgt tcccatagta acgccaatag | | | 180 |
| ggactttcca ttgacgtcaa tgggtggact atttacggta aactgccac ttggcagtac | | | 240 |
| atcaagtgtta tcatatgccca agtacgcccc ctattgacgt caatgacggt aaatggcccg | | | 300 |

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| cctggcatta tgcccagtac atgaccttat gggacttcc tacttggcag tacatctacg | 360 |
| tattagtcat cgctattacc atgggtcgag gtgagccccca cgttctgctt cactctcccc | 420 |
| atctcccccc cctccccacc cccaattttg tatttattha ttttttaattt atttttgtca | 480 |
| gcgatggggg cggggggggg gggggcgcbc gccaggcggg gggggggggg gcgagggcgc | 540 |
| gggcggggcgc aggccggagag gtgcggcgcc agccaatcag agcggcgccgc tccgaaagtt | 600 |
| tcctttatg gcgaggcgcc ggcggcgccgc gccctataaa aagcgaagcg cgccggggcgc | 660 |
| gggagtcgt gcgttgccctt cgcgggtgc cccgctccgc gccgcctcgc gccgcggcgc | 720 |
| cgggctctga ctgaccgcgt tactcccaca ggtgagcggg cgggacggcc cttctccctcc | 780 |
| gggctgtaat tagcgcttgg tttaatgacg gtcgtttct tttctgtggc tgcgtgaaag | 840 |
| ccttaaaggc ctccgggagg gcccgggtgc cgggggggag cggctcgccgg ggtgcgtgcgc | 900 |
| tgtgtgtgtg cgtggggagc gccgcgtgcg gcccgcgtg cccggcgccgt gtgagcgctg | 960 |
| cgggcgcggc ggggggctt gtgcgtcccg cgtgtgcgcg aggggagcgc ggcggggggc | 1020 |
| ggtgccccgc ggtgcggggg ggctgcgagg ggaacaaagg ctgcgtgcgg ggtgtgtgcg | 1080 |
| tgggggggtg agcaggggt gtggcgccgg cggtcggct gtaacccccc cctgcacccc | 1140 |
| cctccccgag ttgcgtgacca cggcccggtc tcgggtgcgg ggctccgtgc gggcgtggc | 1200 |
| gcggggctcg ccgtgcgggg cgggggggtgg cggcaggtgg gggtgccggg cggggcgggg | 1260 |
| ccgcctcggt cgggggaggg ctcggggagag gggcgcggcgc gccccggagc gccggcgccgt | 1320 |
| gtcgaggcgc ggcgagccgc agccattgcc ttttatggta atcgtgcgag agggcgcagg | 1380 |

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| cgtgcgtcgc cgcccgccg tccccttctc catctccagc ctcgggctg ccgcaggggg | 1560 |
| acggctgcct tcggggggga cggggcaggg cggggttcgg ctctggcgt gtgaccggcg | 1620 |
| gctctagagc ctctgctaac catgttcatg cttttctt tttcctacag ctctggca | 1680 |
| acgtgcttgt tgtttgctg tctcatcatt ttggcaaaga attcctcgag gaattcactc | 1740 |
| ctcaggtgca ggctgcctat cagaagggtgg tggctggtgt gccaaatgcc ctggctcaca | 1800 |
| aataccactg agatttttt ccctctgcca aaaattatgg ggacatcatg aagccccttg | 1860 |
| agcatctgac ttctggctaa taaaggaat ttatttcat tgcaatagtg tgttgaaatt | 1920 |
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| agtatttttgt ttagagtttgc acaacatatg ccatatgctg gctgccatga acaaagggtgg | 2040 |
| ctataaagag gtcatcagta tatgaaacag cccctgctg tccattcctt attccataga | 2100 |
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| ctcccagtca tagtgtccc tcttctctta tgaagatccc tcgacctgca gcccaagctt | 2280 |
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| cacattaatt gcgttgcgtc cactgcccgc tttccagtcg ggaaacctgt cgtgccagcg | 2460 |

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| gatccgcata tcaattagtc agcaaccata gtccccccc taactccgcc catccggcc | 2520 |
| ctaaactccgc ccagttccgc ccattctccg ccccatggct gactaatttt ttttatttat | 2580 |
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| aaagcaatag catcacaaat ttcacaaata aagcattttt ttcaactgcat tctagttgt | 2760 |
| gtttgtccaa actcatcaat gtatcttac atgtctggat cogctgcatt aatgaatcgg | 2820 |
| ccaacgcgcg gggagaggcg gtttgcgtat tggcgctct tccgcttcc cgctcaactga | 2880 |
| ctcgctgcgc tcggcgttc ggctgcggcg agcggtatca gctcaactcaa aggcgtaat | 2940 |
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| aaaggccagg aaccgtaaaa aggccgcgtt gctggcgaaa ttccataggc tccggccccc | 3060 |
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| cgttcagtgg aacgaaaact cacgttaagg gatttggtc atgagattat caaaaaggat | 3720 |
| cttcacccatg atcctttaa attaaaaatg aagttttaaa tcaatctaaa gtatatatga | 3780 |
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| tctatccatgt tcacccatag ttgcctgact ccccgctgt tagataacta cgatacggga | 3900 |
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| agatttatca gcaataaacc agccagccgg aaggcccgag cgccagaatg gtcctgcaac | 4020 |
| tttatccogcc tccatccagt ctattaattt tgccggaa gctagagtaa gtagttcgcc | 4080 |
| agttaatagt ttgcgcaacg ttgttgccat tgctacaggc atcgtggtgt cacgctcgcc | 4140 |
| gtttggatgt gcttcattca gctccggttc ccaacgatca aggccgatca catgatcccc | 4200 |
| catgttgtgc aaaaaagcgg ttagctcctt cggccctccg atcgttgtca gaagtaagtt | 4260 |
| ggccgcagtg ttatcactca tggttatggc agcaactgcat aattctctta ctgtcatgcc | 4320 |
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| tatgcggcga ccgagttgtctt cttggccggc gtcaatacgg gataataccg cgccacatag | 4440 |
| cagaacttta aaagtgcgtca tcattggaaa acgttcttgc gggcgaaaac tctcaaggat | 4500 |
| cttaccgctg ttgagatcca gttcgatgtt acccactcgt gcacccaaact gatcttcagc | 4560 |
| atcttttact ttcaccagcg tttctgggtg agcaaaaaca ggaaggcaaa atgcgc当地 | 4620 |

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aaagggaata agggcgacac ggaaatgtt aatactata ctttcctt ttcaatatta 4680

ttgaaggcatt ttcagggtt attgtctcat gagcggatac atatttgaat gtattttagaa 4740

aaataaaacaa atagggttc cgccacatt tccccgaaaa gtgccacctg 4790

<210> 4

<211> 1233

<212> DNA

<213> Artificial Sequence

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<222> (13)..(1224)

<223> DNA insert encoding rat CTLA4, rat IgG Fc region and glucagon C19-29 region

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Met Ala Cys Leu Gly Leu Gln Arg Tyr Lys Thr His Leu

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5

10

cag ctg cct tct agg act tgg cct ttt gga gtc ctg ctt tct ctt ctc 99

Gln Leu Pro Ser Arg Thr Trp Pro Phe Gly Val Leu Leu Ser Leu Leu

15

20

25

ttc atc cca atc ttc tct gaa gcc ata caa gtg acc caa cct tca gtg 147

Phe Ile Pro Ile Phe Ser Glu Ala Ile Gln Val Thr Gln Pro Ser Val

30

35

40

45

gtg ttg gcc agc agc cac ggt gtc gcc agc ttt cca tgt gaa tat goa 195

Val Leu Ala Ser Ser His Gly Val Ala Ser Phe Pro Cys Glu Tyr Ala

50

55

60

tct tca cac aac act gat gag gtc cgg gtg acg gtg ctg cgg cag aca 243

Ser Ser His Asn Thr Asp Glu Val Arg Val Thr Val Leu Arg Gln Thr

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65

70

75

aat gac caa gtg aca gag gtc tgt gcc acg aca ttc aca gtg aag aac 291

Asn Asp Gln Val Thr Glu Val Cys Ala Thr Thr Phe Thr Val Lys Asn

80

85

90

acg ttg ggc ttc cta gat gac ccc ttc tgc agt ggt acc ttt aat gaa 339

Thr Leu Gly Phe Leu Asp Asp Pro Phe Cys Ser Gly Thr Phe Asn Glu

95

100

105

agc aga gtg aac ctc acc atc caa gga ctg agg gct gac acc gga 387

Ser Arg Val Asn Leu Thr Ile Gln Gly Leu Arg Ala Ala Asp Thr Gly

110

115

120

125

ctg tac ttc tgc aag gtg gaa ctc atg tac cca ccg cca tac ttt gtg 435

Leu Tyr Phe Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr Phe Val

130

135

140

ggc atg ggc aac ggg acc cag att tat gtc atc gat cca gaa cca tgc 483

Gly Met Gly Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys

145

150

155

cca gat tca gac gcg gcc gcc gtg ccc aga aac tgt gga ggt gat tgc 531

Pro Asp Ser Asp Ala Ala Val Pro Arg Asn Cys Gly Gly Asp Cys

160

165

170

aag cct tgt ata tgt aca ggc tca gaa gta tca tct gtc ttc atc ttc 579

Lys Pro Cys Ile Cys Thr Gly Ser Glu Val Ser Ser Val Phe Ile Phe

175

180

185

ccc cca aag ccc aaa gat gtg ctc acc atc act ctg act cct aag gtc 627

Pro Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr Pro Lys Val

190

195

200

205

acg tgt gtt gtg gta gac att agc cag gac gat ccc gag gtc cat ttc 675

Thr Cys Val Val Val Asp Ile Ser Gln Asp Asp Pro Glu Val His Phe

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210

215

220

agc tgg ttt gta gat gac gtg gaa gtc cac aca gct cag act cga cca 723
Ser Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln Thr Arg Pro

225

230

235

cca gag gag cag ttc aac agc act ttc cgc tca gtc agt gaa ctc ccc 771
Pro Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser Glu Leu Pro

240

245

250

atc ctg cac cag gac tgg ctc aat ggc agg acg ttc aga tgc aag gtc 819
Ile Leu His Gln Asp Trp Leu Asn Gly Arg Thr Phe Arg Cys Lys Val

255

260

265

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Thr Ser Ala Ala Phe Pro Ser Pro Ile Glu Lys Thr Ile Ser Lys Pro
270 275 280 285

gaa ggc aga aca caa gtt ccg cat gta tac acc atg tca cct acc aag 915
Glu Gly Arg Thr Gln Val Pro His Val Tyr Thr Met Ser Pro Thr Lys
290 295 300

gaa gag atg acc cag aat gaa gtc agt atc acc tgc atg gta aaa ggc 963
Glu Glu Met Thr Gln Asn Glu Val Ser Ile Thr Cys Met Val Lys Gly
305 310 315

ttc tat ccc cca gac att tat gtg gag tgg cag atg aac ggg cag cca 1011
Phe Tyr Pro Pro Asp Ile Tyr Val Glu Trp Gln Met Asn Gly Gln Pro
320 325 330

cag gaa aac tac aag aac act cca cct acg atg gac aca gat ggg agt 1059
Gln Glu Asn Tyr Lys Asn Thr Pro Pro Thr Met Asp Thr Asp Gly Ser
335 340 345

tac ttc ctc tac agc aag ctc aat gtg aag aag gaa aaa tgg cag cag 1107
Tyr Phe Leu Tyr Ser Lys Leu Asn Val Lys Lys Glu Lys Trp Gln Gln

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|--|-----|-----|-----|------|
| 350 | 355 | 360 | 365 | |
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| 370 | 375 | 380 | | 1155 |
| cat act gag aag agt ctc tcc cac tct ccg ggt aaa gcc caa gat ttt His Thr Glu Lys Ser Leu Ser His Ser Pro Gly Lys Ala Gln Asp Phe | | | | |
| 385 | 390 | 395 | | 1203 |
| gtg cag tgg ttg atg aat acc tgagaattc Val Gln Trp Leu Met Asn Thr | | | | |
| 400 | | | | 1233 |
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| <213> Artificial Sequence | | | | |
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| <221> CDS | | | | |
| <222> (13)..(1134) | | | | |
| <223> DNA insert encoding rat IL13, rat IgG Fc region and glucagon C19-29 region | | | | |
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| 1 | 5 | 10 | | |
| ctt ggt ggt ctt gcc acc cca ggg cca gtg cgg aga tcc aca tct ccc 99 Leu Gly Gly Leu Ala Thr Pro Gly Pro Val Arg Arg Ser Thr Ser Pro | | | | |
| 15 | 20 | 25 | | |
| cct gtg gcc ctc agg gag ctt atc gag gag ctg agc aac atc aca caa 147 Pro Val Ala Leu Arg Glu Leu Ile Glu Glu Leu Ser Asn Ile Thr Gln | | | | |
| 30 | 35 | 40 | 45 | |

| | | | |
|---|-----|-----|-----|
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| Asp Gln Lys Thr Ser Leu Cys Asn Ser Ser Met Val Trp Ser Val Asp | | | |
| 50 | 55 | 60 | |
| ctg aca gct ggc ggg ttc tgt gca gcc ctg gaa tcc ctg acc aac atc | | | 243 |
| Leu Thr Ala Gly Gly Phe Cys Ala Ala Leu Glu Ser Leu Thr Asn Ile | | | |
| 65 | 70 | 75 | |
| tcc agt tgc aat gcc atc cac agg acc cag agg ata ttg aat ggc ctc | | | 291 |
| Ser Ser Cys Asn Ala Ile His Arg Thr Gln Arg Ile Leu Asn Gly Leu | | | |
| 80 | 85 | 90 | |
| tgt aac caa aag gcc tcg gat gtg gct tcc agc ccc cca gat acc aaa | | | 339 |
| Cys Asn Gln Lys Ala Ser Asp Val Ala Ser Ser Pro Pro Asp Thr Lys | | | |
| 95 | 100 | 105 | |
| atc gaa gta gcc cag ttt ata tca aaa ctg ctc aat tac tcc aag caa | | | 387 |
| Ile Glu Val Ala Gln Phe Ile Ser Lys Leu Leu Asn Tyr Ser Lys Gln | | | |
| 110 | 115 | 120 | 125 |
| ctt ttc cgc tat ggc cac gcg gcc gtg ccc aga aac tgt gga ggt | | | 435 |
| Leu Phe Arg Tyr Gly His Ala Ala Ala Val Pro Arg Asn Cys Gly Gly | | | |
| 130 | 135 | 140 | |
| gat tgc aag cct tgt ata tgt aca ggc tca gaa gta tca tct gtc ttc | | | 483 |
| Asp Cys Lys Pro Cys Ile Cys Thr Gly Ser Glu Val Ser Ser Val Phe | | | |
| 145 | 150 | 155 | |
| atc ttc ccc cca aag ccc aaa gat gtg ctc acc atc act ctg act cct | | | 531 |
| Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr Pro | | | |
| 160 | 165 | 170 | |
| aag gtc acg tgt gtt gtg gta gac att agc cag gac gat ccc gag gtc | | | 579 |
| Lys Val Thr Cys Val Val Val Asp Ile Ser Gln Asp Asp Pro Glu Val | | | |
| 175 | 180 | 185 | |

| | | |
|---|-----|------|
| cat ttc agc tgg ttt gta gat gac gtg gaa gtc cac aca got cag act | | 627 |
| His Phe Ser Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln Thr | | |
| 190 | 195 | 200 |
| | | 205 |
| cga cca cca gag gag cag ttc aac agc act ttc cgc tca gtc agt gaa | | 675 |
| Arg Pro Pro Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser Glu | | |
| 210 | 215 | 220 |
| ctc ccc atc ctg cac cag gac tgg ctc aat ggc agg acg ttc aga tgc | | 723 |
| Leu Pro Ile Leu His Gln Asp Trp Leu Asn Gly Arg Thr Phe Arg Cys | | |
| 225 | 230 | 235 |
| aag gtc acc agt gca gct ttc cca tcc ccc atc gag aaa acc atc tcc | | 771 |
| Lys Val Thr Ser Ala Ala Phe Pro Ser Pro Ile Glu Lys Thr Ile Ser | | |
| 240 | 245 | 250 |
| aaa ccc gaa ggc aga aca caa gtt ccg cat gta tac acc atg tca cct | | 819 |
| Lys Pro Glu Gly Arg Thr Gln Val Pro His Val Tyr Thr Met Ser Pro | | |
| 255 | 260 | 265 |
| acc aag gaa gag atg acc cag aat gaa gtc agt atc acc tgc atg gta | | 867 |
| Thr Lys Glu Glu Met Thr Gln Asn Glu Val Ser Ile Thr Cys Met Val | | |
| 270 | 275 | 280 |
| | | 285 |
| aaa ggc ttc tat ccc cca gac att tat gtg gag tgg cag atg aac ggg | | 915 |
| Lys Gly Phe Tyr Pro Pro Asp Ile Tyr Val Glu Trp Gln Met Asn Gly | | |
| 290 | 295 | 300 |
| cag cca cag gaa aac tac aag aac act cca cct acg atg gac aca gat | | 963 |
| Gln Pro Gln Glu Asn Tyr Lys Asn Thr Pro Pro Thr Met Asp Thr Asp | | |
| 305 | 310 | 315 |
| ggg agt tac ttc ctc tac agc aag ctc aat gtg aag aag gaa aaa tgg | | 1011 |
| Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Asn Val Lys Lys Glu Lys Trp | | |
| 320 | 325 | 330 |

cag cag gga aac acg ttc acg tgt tct gtg ctg cat gaa ggc ctg cac 1059
 Gln Gln Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu His
 335 340 345

aac cac cat act gag aag agt ctc tcc cac tct ccg ggt aaa gcc caa 1107
 Asn His His Thr Glu Lys Ser Leu Ser His Ser Pro Gly Lys Ala Gln
 350 355 360 365

gat ttt gtg cag tgg ttg atg aat acc tgagaattc 1143
 Asp Phe Val Gln Trp Leu Met Asn Thr
 370

<210> 6
<211> 825
<212> DNA
<213> Artificial Sequence
<220>
<221> CDS
<222> (13)..(816)
<223> DNA insert encoding rat signal peptide, rat IgG Fc region and glucagon C19-29
region

<400> 6
gaattcattt aa atg aag tcc tgc ggc ctg ttc cct ctc atg gtg ctc ctt 51
Met Lys Ser Cys Gly Leu Phe Pro Leu Met Val Leu Leu
1 5 10

gct ctg ggt gta ctg gca ccc tgg agt gtg gaa gga gcg gcc ggc gtg 99
Ala Leu Gly Val Leu Ala Pro Trp Ser Val Glu Gly Ala Ala Ala Val
15 20 25

ccc aga aac tgt gga ggt gat tgc aag cct tgt ata tgt aca ggc tca 147
Pro Arg Asn Cys Gly Gly Asp Cys Lys Pro Cys Ile Cys Thr Gly Ser
30 35 40 45

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| | | | |
|---|-----|-----|-----|
| gaa gta tca tct gtc ttc atc ttc ccc cca aag ccc aaa gat gtg ctc | 195 | | |
| Glu Val Ser Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu | | | |
| 50 | 55 | 60 | |
| acc atc act ctg act cct aag gtc acg tgt gtt gtg gta gac att agc | 243 | | |
| Thr Ile Thr Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile Ser | | | |
| 65 | 70 | 75 | |
| cag gac gat ccc gag gtc cat ttc agc tgg ttt gta gat gac gtg gaa | 291 | | |
| Gln Asp Asp Pro Glu Val His Phe Ser Trp Phe Val Asp Asp Val Glu | | | |
| 80 | 85 | 90 | |
| gtc cac aca gct cag act cga cca cca gag gag cag ttc aac agc act | 339 | | |
| Val His Thr Ala Gln Thr Arg Pro Pro Glu Glu Gln Phe Asn Ser Thr | | | |
| 95 | 100 | 105 | |
| ttc cgc tca gtc agt gaa ctc ccc atc ctg cac cag gac tgg ctc aat | 387 | | |
| Phe Arg Ser Val Ser Glu Leu Pro Ile Leu His Gln Asp Trp Leu Asn | | | |
| 110 | 115 | 120 | 125 |
| ggc agg acg ttc aga tgc aag gtc acc agt gca gct ttc cca tcc ccc | 435 | | |
| Gly Arg Thr Phe Arg Cys Lys Val Thr Ser Ala Ala Phe Pro Ser Pro | | | |
| 130 | 135 | 140 | |
| atc gag aaa acc atc tcc aaa ccc gaa ggc aga aca caa gtt ccg cat | 483 | | |
| Ile Glu Lys Thr Ile Ser Lys Pro Glu Gly Arg Thr Gln Val Pro His | | | |
| 145 | 150 | 155 | |
| gta tac acc atg tca cct acc aag gaa gag atg acc cag aat gaa gtc | 531 | | |
| Val Tyr Thr Met Ser Pro Thr Lys Glu Glu Met Thr Gln Asn Glu Val | | | |
| 160 | 165 | 170 | |
| agt atc acc tgc atg gta aaa ggc ttc tat ccc cca gac att tat gtg | 579 | | |
| Ser Ile Thr Cys Met Val Lys Gly Phe Tyr Pro Pro Asp Ile Tyr Val | | | |
| 175 | 180 | 185 | |

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gag tgg cag atg aac ggg cag cca cag gaa aac tac aag aac act cca 627
Glu Trp Gln Met Asn Gly Gln Pro Gln Glu Asn Tyr Lys Asn Thr Pro
190 195 200 205

cct acg atg gac aca gat ggg agt tac ttc ctc tac agc aag ctc aat 675
Pro Thr Met Asp Thr Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Asn
210 215 220

gtg aag aag gaa aaa tgg cag cag gga aac acg ttc acg tgt tct gtg 723
Val Lys Lys Glu Lys Trp Gln Gln Gly Asn Thr Phe Thr Cys Ser Val
225 230 235

ctg cat gaa ggc ctg cac aac cac cat act gag aag agt ctc tcc cac 771
Leu His Glu Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser His
240 245 250

tct ccg ggt aaa gcc caa gat ttt gtg cag tgg ttg atg aat acc 816
Ser Pro Gly Lys Ala Gln Asp Phe Val Gln Trp Leu Met Asn Thr
255 260 265

tgagaattc 825

<210> 7

<211> 1284

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (13)..(1275)

<223> DNA insert encoding rat IL1 receptor antagonist, rat IgG Fc region and glucagon C19-29 region

<400> 7

gaattcattt aa atg gaa atc tgc tgg gga ccc tac agt cac cta atc tct 51

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| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Ile | Cys | Trp | Gly | Pro | Tyr | Ser | His | Leu | Ile | Ser | | | | |
| 1 | | | | | | | | | | | | | 10 | | | |
| ctc | ctt | ctc | atc | ctt | ctg | ttt | cat | tca | gag | gca | gcc | tgc | cgc | cct | tct | 99 |
| Leu | Leu | Leu | Ile | Leu | Leu | Phe | His | Ser | Glu | Ala | Ala | Cys | Arg | Pro | Ser | |
| 15 | | | | | | | | | | | | | | 25 | | |
| ggg | aaa | aga | ccc | tgc | aag | atg | caa | gcc | ttc | aga | atc | tgg | gat | act | aac | 147 |
| Gly | Lys | Arg | Pro | Cys | Lys | Met | Gln | Ala | Phe | Arg | Ile | Trp | Asp | Thr | Asn | |
| 30 | | | | | | | | | | | | | | 45 | | |
| cag | aag | acc | ttt | tac | ctg | aga | aac | aac | cag | ctc | att | gct | ggg | tac | tta | 195 |
| Gln | Lys | Thr | Phe | Tyr | Leu | Arg | Asn | Asn | Gln | Leu | Ile | Ala | Gly | Tyr | Leu | |
| 50 | | | | | | | | | | | | | | 60 | | |
| caa | gga | cca | aat | atc | aaa | cta | gaa | gaa | aag | ata | gac | atg | gtg | cct | att | 243 |
| Gln | Gly | Pro | Asn | Ile | Lys | Leu | Glu | Glu | Lys | Ile | Asp | Met | Val | Pro | Ile | |
| 65 | | | | | | | | | | | | | | 75 | | |
| gac | ctt | cat | agt | gtg | ttc | ttg | ggc | atc | cac | ggg | ggc | aag | ctg | tgc | ctg | 291 |
| Asp | Leu | His | Ser | Val | Phe | Leu | Gly | Ile | His | Gly | Gly | Lys | Leu | Cys | Leu | |
| 80 | | | | | | | | | | | | | | 90 | | |
| tct | tgt | gcc | aag | tct | gga | gat | gat | atc | aag | ctc | cag | ctg | gag | gaa | gtt | 339 |
| Ser | Cys | Ala | Lys | Ser | Gly | Asp | Asp | Ile | Lys | Leu | Gln | Leu | Glu | Glu | Val | |
| 95 | | | | | | | | | | | | | | 105 | | |
| aac | atc | act | gat | ctg | agc | aag | aac | aaa | gaa | gaa | gac | aag | cgc | ttt | acc | 387 |
| Asn | Ile | Thr | Asp | Leu | Ser | Lys | Asn | Lys | Glu | Glu | Asp | Lys | Arg | Phe | Thr | |
| 110 | | | | | | | | | | | | | | 125 | | |
| ttc | atc | cgc | tct | gag | aaa | ggc | ccc | acc | acc | agc | ttt | gag | tca | gct | gcc | 435 |
| Phe | Ile | Arg | Ser | Glu | Lys | Gly | Pro | Thr | Thr | Ser | Phe | Glu | Ser | Ala | Ala | |
| 130 | | | | | | | | | | | | | | 140 | | |
| tgt | cca | gga | tgg | ttc | ctc | tgc | aca | aca | cta | gag | gct | gac | cgt | cct | gtg | 483 |

| | | | |
|---|-----|-----|-----|
| Cys Pro Gly Trp Phe Leu Cys Thr Thr Leu Glu Ala Asp Arg Pro Val | | | |
| 145 | 150 | 155 | |
| agc ctc acc aac aca ccg gaa gag ccc ctt ata gtc acg aag ttc tac | | | 531 |
| Ser Leu Thr Asn Thr Pro Glu Glu Pro Leu Ile Val Thr Lys Phe Tyr | | | |
| 160 | 165 | 170 | |
| ttc cag gaa gac caa gcg gcc gcc gtg ccc aga aac tgt gga ggt gat | | | 579 |
| Phe Gln Glu Asp Gln Ala Ala Ala Val Pro Arg Asn Cys Gly Gly Asp | | | |
| 175 | 180 | 185 | |
| tgc aag cct tgt ata tgt aca ggc tca gaa gta tca tct gtc ttc atc | | | 627 |
| Cys Lys Pro Cys Ile Cys Thr Gly Ser Glu Val Ser Ser Val Phe Ile | | | |
| 190 | 195 | 200 | 205 |
| ttc ccc cca aag ccc aaa gat gtg ctc acc atc act ctg act cct aag | | | 675 |
| Phe Pro Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr Pro Lys | | | |
| 210 | 215 | 220 | |
| gtc acg tgt gtt gtg gta gac att agc cag gac gat ccc gag gtc cat | | | 723 |
| Val Thr Cys Val Val Val Asp Ile Ser Gln Asp Asp Pro Glu Val His | | | |
| 225 | 230 | 235 | |
| ttc agc tgg ttt gta gat gac gtg gaa gtc cac aca gct cag act cga | | | 771 |
| Phe Ser Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln Thr Arg | | | |
| 240 | 245 | 250 | |
| cca cca gag gag cag ttc aac agc act ttc cgc tca gtc agt gaa ctc | | | 819 |
| Pro Pro Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser Glu Leu | | | |
| 255 | 260 | 265 | |
| ccc atc ctg cac cag gac tgg ctc aat ggc agg acg ttc aga tgc aag | | | 867 |
| Pro Ile Leu His Gln Asp Trp Leu Asn Gly Arg Thr Phe Arg Cys Lys | | | |
| 270 | 275 | 280 | 285 |
| gtc acc agt gca gct ttc cca tcc ccc atc gag aaa acc atc tcc aaa | | | 915 |

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Val Thr Ser Ala Ala Phe Pro Ser Pro Ile Glu Lys Thr Ile Ser Lys
290 295 300

ccc gaa ggc aga aca caa gtt ccg cat gta tac acc atg tca cct acc 963
Pro Glu Gly Arg Thr Gln Val Pro His Val Tyr Thr Met Ser Pro Thr
305 310 315

aag gaa gag atg acc cag aat gaa gtc agt atc acc tgc atg gta aaa 1011
Lys Glu Glu Met Thr Gln Asn Glu Val Ser Ile Thr Cys Met Val Lys
320 325 330

ggc ttc tat ccc cca gac att tat gtg gag tgg cag atg aac ggg cag 1059
Gly Phe Tyr Pro Pro Asp Ile Tyr Val Glu Trp Gln Met Asn Gly Gln
335 340 345

cca cag gaa aac tac aag aac act cca cct acg atg gac aca gat ggg 1107
Pro Gln Glu Asn Tyr Lys Asn Thr Pro Pro Thr Met Asp Thr Asp Gly
350 355 360 365

agt tac ttc ctc tac agc aag ctc aat gtg aag aag gaa aaa tgg cag 1155
Ser Tyr Phe Leu Tyr Ser Lys Leu Asn Val Lys Lys Glu Lys Trp Gln
370 375 380

cag gga aac acg ttc acg tgt tct gtg ctg cat gaa ggc ctg cac aac 1203
Gln Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu His Asn
385 390 395

cac cat act gag aag agt ctc tcc cac tct ccg ggt aaa gcc caa gat 1251
His His Thr Glu Lys Ser Leu Ser His Ser Pro Gly Lys Ala Gln Asp
400 405 410

ttt gtg cag tgg ttg atg aat acc tgagaattc 1284
Phe Val Gln Trp Leu Met Asn Thr
415 420

<210> 8
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (13)..(360)
<223> DNA insert encoding human IL8 and glucagon C19-29 region

<400> 8

gaattcattt aa atg act tcc aag ctg gcc gtg gct ctc ttg gca gcc ttc 51
Met Thr Ser Lys Leu Ala Val Ala Leu Leu Ala Ala Phe
1 5 10

ctg att tct gca gct ctg tgt gaa ggt gca gtt ttg cca agg agt gct 99
Leu Ile Ser Ala Ala Leu Cys Glu Gly Ala Val Leu Pro Arg Ser Ala
15 20 25

aaa gaa ctt aga tgt cag tgc ata aag aca tac tcc aaa cct ttc cac 147
 Lys Glu Leu Arg Cys Gln Cys Ile Lys Thr Tyr Ser Lys Pro Phe His
 30 35 40 45

ccc aaa ttt atc aaa gaa ctg aga gtg att gag agt gga cca cac tgc 195
 Pro Lys Phe Ile Lys Glu Leu Arg Val Ile Glu Ser Gly Pro His Cys
 50 55 60

gcc aac aca gaa att att gta aag ctt tct gat gga aga gag ctc tgt 243
Ala Asn Thr Glu Ile Ile Val Lys Leu Ser Asp Gly Arg Glu Leu Cys
65 70 75

ctg gac ccc aag gaa aac tgg gtg cag agg gtt gtg gag aag ttt ttg 291
 Leu Asp Pro Lys Glu Asn Trp Val Gln Arg Val Val Glu Lys Phe Leu
 80 85 90

aag agg gct gag aat tca gcg gcc gcc ccg ggt aaa gcc caa gat ttt 339

Lys Arg Ala Glu Asn Ser Ala Ala Ala Pro Gly Lys Ala Gln Asp Phe
 95 100 105

gtg cag tgg ttg atg aat acc tgagaattc 369
 Val Gin Trp Leu Met Asn Thr
 110 115

<210> 9
 <211> 45
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Oligonucleotide primer used for constructing a vector pCAGGS-IgG-glu19-29

<400> 9
 gagaattcat ttaaatgaga gcggccgcgcg tgcccagaaa ctgtg 45

<210> 10
 <211> 49
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Oligonucleotide primer used for constructing a vector pCAGGS-IgG-glu19-29

<400> 10
 tcaaccactg cacaaaatct tgggctttac ccggagagtg ggagagact 49

<210> 11
 <211> 45
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Oligonucleotide primer used for constructing a vector pCAGGS-IgG-glu19-29

<400> 11

gagaattcat ttaaatgaga gcggccgccc tgcccagaaa ctgtg

45

<210> 12

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer used for constructing a vector pCAGGS-IgG-glu19-29

<400> 12

gagagagaga attctcaggt attcatcaac cactgcacaa aatcttggc

50

<210> 13

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer used for constructing a vector
pCAGGS-IFN-rR-IgG-glu19-29

<400> 13

gagaattcat ttaaatgatt ctgctggtgg tcctgatg

38

<210> 14

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer used for constructing a vector
pCAGGS-IFN-rR-IgG-glu19-29

25/28

<400> 14

gcagcatcgccggccgcttctctctgtcatcatggagaaa

40

<210> 15

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer used for constructing a vector
pCAGGS-CTLA4-IgG-glu19-29

<400> 15

gagaattcat ttaaatggct tgtcttggac tccagagg

38

<210> 16

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer used for constructing a vector
pCAGGS-CTLA4-IgG-glu19-29

<400> 16

gcagcatcgccggccgctctaatctgggc atggttctgg

40

<210> 17

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer used for constructing a vector
pCAGGS-IL13-IgG-glu19-29

<400> 17

gagaattcat ttaaatggca ctctgggtga ctgcagtc

38

<210> 18

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer used for constructing a vector
pCAGGS-IL13-IgG-glu19-29

<400> 18

gcagccatcgcc ggccgcgtgg ccatagcgga aaagttgctt

40

<210> 19

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer used for constructing a vector
pCAGGS-IL1RA-IgG-glu19-29

<400> 19

gagaattcat ttaaatggaa atctgctggg gaccctac

38

<210> 20

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer used for constructing a vector
pCAGGS-IL1RA-IgG-glu19-29

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<400> 20

gcagcatcgccgcgcgttgg tcttcctgga agtagaaactt

40

<210> 21

<211> 62

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer used for constructing a vector pCAGGS-glu19-29

<400> 21

gagaattcat ttaaatgaga gcggccgc cggtaaagc ccaagattt gtgcagtgg 60

tg 62

<210> 22

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer used for constructing a vector pCAGGS-glu19-29

<400> 22

gagagagaga attctcaggt attcatcaac cactgcacaa aatcttggc

50

<210> 23

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer used for constructing a vector pCAGGS-IL8-glu19-29

<400> 23

gagaattcat ttaaatgact tccaagctgg ccgtggc

38

<210> 24

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer used for constructing a vector pCAGGS-IL8-glu19-29

<400> 24

gcagcatcgccggccgctgaa ttctcagccc tcttcaaaaa

40